SEQUENCE LISTING

<110> University of Rochester
McCance, Dennis
Westbrook, III, Thomas F.

<120> E7 REGULATION OF P21^{CIP1} THROUGH AKT

<130> 21108.0016P1

<150> 60/374,245
<151> 2002-04-19

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 1

Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser
1				5					10					15	
His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu
			20					25					30		
Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro
		35					40					45			
Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg
	50					55					60				
Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg
65					70					75					80
Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met
				85					90					95	
Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn
			100					105					110		
Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg
		115					120					125			
Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu
	130					135					140				
Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys
145					150					155					160
Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys
				165					170					175	
Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu
			180					185					190		
Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg
		195					200					205			
Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala
	210					215					220				
Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met
225					230					235					240

Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln
245 250 255
Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr
260 265 270
Gln

<210> 2
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 2
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
1 5 10 15
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
20 25 30
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
35 40 45
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
50 55 60
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
65 70 75 80
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
85 90 95
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
100 105 110
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
115 120 125
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
130 135 140
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
145 150 155 160
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
165 170 175
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
180 185 190
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
195 200 205
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
210 215 220
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
225 230 235 240
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
245 250 255
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
260 265 270
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
275 280 285
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
290 295 300
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
305 310 315 320
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
325 330 335

Thr Ser Pro Arg Leu Pro Val Phe
340

<210> 3
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 3
Lys Met Ser Lys Asp Gly Lys Lys Lys Lys Lys Lys Thr Lys Thr Lys
1 5 10 15
Cys Ile Ile Met
20

<210> 4
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 4
Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
1 5 10 15
Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Arg Arg
20 25 30
Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
35 40 45
Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
50 55 60
Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
65 70 75 80
Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
85 90 95
Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
100 105 110
Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
115 120 125
Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
130 135 140
Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
145 150 155 160
Lys Arg Lys Pro

<210> 5
<211> 495
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 5
atgtcagaac cggctgggga tgtccgtcag aacccatgcg gcagcaaggc ctgccgccgc 60
ctcttcggcc cagtggacag cgagcagctg agccgcgact gtgatgcgct aatggcgggc 120
tgcatccagg aggcccgtga gcgatggaac ttcgactttg tcaccgagac accactggag 180
ggtgacttcg cctgggagcg tgtgcggggc cttggcctgc ccaagctcta ccttcccacg 240
gggccccggc gaggccggga tgagttggga ggaggcaggc ggcctggcac ctcacctgct 300
ctgctgcagg ggacagcaga ggaagaccat gtggacctgt cactgtcttg tacccttgtg 360
cctcgctcag gggagcaggc tgaagggtcc ccaggtggac ctggagactc tcagggtcga 420
aaacggcggc agaccagcat gacagatttc taccactcca aacgccggct gatcttctcc 480
aagaggaagc cctaa 495

<210> 6
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 6
Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
1 5 10 15
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
20 25 30
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
35 40 45
Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
50 55 60
Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65 70 75 80
Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
85 90 95
Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
100 105 110
Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
115 120 125
Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
130 135 140
Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
145 150 155 160
Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
165 170 175
Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
180 185 190
Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
195 200 205
Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
210 215 220
Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
225 230 235 240
Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
245 250 255
Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr
260 265 270
Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile
275 280 285

```
Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala
    290                 295                 300
Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val
305                 310                 315                 320
Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly
                325                 330                 335
Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln
            340                 345                 350
Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe
        355                 360                 365
Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu
    370                 375                 380
Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys
385                 390                 395                 400
Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val
                405                 410                 415
Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu
            420                 425                 430
Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr
        435                 440                 445
Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu
    450                 455                 460
Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala
465                 470                 475                 480
```

<210> 7
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 7

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atgagcgacg tggctattgt gaaggagggt tggctgcaca aacgagggga gtacatcaag      60
acctggcggc cacgctactt cctcctcaag aatgatggca ccttcattgg ctacaaggag     120
cggccgcagg atgtggacca acgtgaggct cccctcaaca acttctctgt ggcgcagtgc     180
cagctgatga agacggagcg gccccggccc aacaccttca tcatccgctg cctgcagtgg     240
accactgtca tcgaacgcac cttccatgtg gagactcctg aggagcggga ggagtggaca     300
accgccatcc agactgtggc tgacggcctc aagaagcagg aggaggagga gatggacttc     360
cggtcgggct cacccagtga caactcaggg gctgaagaga tggaggtgtc cctggccaag     420
cccaagcacc gcgtgaccat gaacgagttt gagtacctga agctgctggg caagggcact     480
ttcggcaagg tgatcctggt gaaggagaag gccacaggcc gctactacgc catgaagatc     540
ctcaagaagg aagtcatcgt ggccaaggac gaggtggccc acacactcac cgagaaccgc     600
gtcctgcaga actccaggca ccccttcctc acagccctga agtactcttt ccagacccac     660
gaccgcctct gctttgtcat ggagtacgcc aacgggggcg agctgttctt ccacctgtcc     720
cgggaacgtg tgttctccga ggaccgggcc cgcttctatg gcgctgagat tgtgtcagcc     780
ctggactacc tgcactcgga gaagaacgtg gtgtaccggg acctcaagct ggagaacctc     840
atgctggaca aggacgggca cattaagatc acagacttcg ggctgtgcaa ggaggggatc     900
aaggacggtg ccaccatgaa gacctttttgc ggcacacctg agtacctggc ccccgaggtg     960
ctggaggaca atgactacgg ccgtgcagtg gactggtggg ggctgggcgt ggtcatgtac    1020
gagatgatgt gcggtcgcct gcccttctac aaccaggacc atgagaagct ttttgagctc    1080
atcctcatgg aggagatccg cttcccgcgc acgcttggtc ccgaggccaa gtccttgctt    1140
tcagggctgc tcaagaagga ccccaagcag aggcttggcg ggggctccga ggacgccaag    1200
gagatcatgc agcatcgctt ctttgccggt atcgtgtggc agcacgtgta cgagaagaag    1260
ctcagcccac ccttcaagcc ccaggtcacg tcggagactg acaccaggta ttttgatgag    1320
gagttcacgg cccagatgat caccatcaca ccacctgacc aagatgacag catggagtgt    1380
gtggacagcg agcgcaggcc ccacttcccc cagttctcct actcggccag cagcacggcc    1440
```

tga 1443

<210> 8
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 8
Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95
Lys Pro

<210> 9
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 9
atgcatggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact 60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt 120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 10
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 10
atgcacggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact 60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt 120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 11
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 11
Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
1 5 10 15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
20 25 30
Glu Glu Glu Asp Glu Val Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
35 40 45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
50 55 60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65 70 75 80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
85 90 95
Lys Pro

<210> 12
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 12
atgcatggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact 60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt 120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 13
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 13
atgcacggag atacacctac attgcatgaa tatatgttag atttgcaacc agagacaact 60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt 120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 14
<211> 648

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 14
Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
1 5 10 15
Leu Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
20 25 30
Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
35 40 45
Thr Asp Ser Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
50 55 60
Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65 70 75 80
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
85 90 95
Ala Val Phe Arg Leu Leu Gln Glu His Lys Gly Lys Lys Ala Arg Leu
100 105 110
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
115 120 125
Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
130 135 140
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145 150 155 160
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
165 170 175
Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
180 185 190
Leu Leu Leu Phe Pro Asn Ser Thr Ala Ser Asp Ser Gly Val Pro Ala
195 200 205
Pro Pro Ser Phe Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
210 215 220
Pro Ala Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
225 230 235 240
Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
245 250 255
Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
260 265 270
Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
275 280 285
Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
290 295 300
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305 310 315 320
Gly Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
325 330 335
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
340 345 350
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
355 360 365
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
370 375 380
Glu Gln Leu Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385 390 395 400

```
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
                405                 410                 415
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
            420                 425                 430
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
        435                 440                 445
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
    450                 455                 460
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465                 470                 475                 480
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
                485                 490                 495
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
            500                 505                 510
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
        515                 520                 525
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
    530                 535                 540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545                 550                 555                 560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Arg Leu Tyr Lys Asn
                565                 570                 575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
            580                 585                 590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
        595                 600                 605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
    610                 615                 620
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625                 630                 635                 640
Thr Ser Pro Arg Leu Pro Val Phe
                645
```

<210> 15
<211> 2977
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 15

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ccgaatgtga ccgcctcccg ctccctcacc cgccgcgggg aggaggagcg ggcgagaagc      60
tgccgccgaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa     120
gctgcatcaa tggagcacat acagggagct tggaagacga tcagcaatgg ttttggattc     180
aaagatgccg tgtttgatgg ctccagctgc atctctccta caatagttca gcagtttggc     240
tatcagcgcc gggcatcaga tgatggcaaa ctcacagatc cttctaagac aagcaacact     300
atccgtgttt tcttgccgaa caagcaaaga acagtggtca atgtgcgaaa tggaatgagc     360
ttgcatgact gccttatgaa agcactcaag gtgaggggcc tgcaaccaga gtgctgtgca     420
gtgttcagac ttctccacga acacaaaggt aaaaaagcac gcttagattg gaatactgat     480
gctgcgtctt tgattggaga agaacttcaa gtagatttcc tggatcatgt tcccctcaca     540
acacacaact ttgctcggaa gacgttcctg aagcttgcct tctgtgacat ctgtcagaaa     600
ttcctgctca atggatttcg atgtcagact tgtggctaca aatttcatga gcactgtagc     660
accaaagtac ctactatgtg tgtggactgg agtaacatca gacaactctt attgtttcca     720
aattccacta ttggtgatag tggagtccca gcactacctt ctttgactat gcgtcgtatg     780
cgagagtctg tttccaggat gcctgttagt tctcagcaca gatattctac acctcacgcc     840
ttcaccttta acacctccag tccctcatct gaaggttccc tctcccagag gcagaggtcg     900
acatccacac ctaatgtcca catggtcagc accacgctgc ctgtggacag caggatgatt     960
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```
gaggatgcaa ttcgaagtca cagcgaatca gcctcacctt cagccctgtc cagtagcccc    1020
aacaatctga gcccaacagg ctggtcacag ccgaaaaccc ccgtgccagc acaaagagag    1080
cgggcaccag tatctgggac ccaggagaaa aacaaaatta ggcctcgtgg acagagagat    1140
tcaagctatt attgggaaat agaagccagt gaagtgatgc tgtccactcg gattgggtca    1200
ggctcttttg gaactgttta taagggtaaa tggcacggag atgttgcagt aaagatccta    1260
aaggttgtcg acccaacccc agagcaattc caggccttca ggaatgaggt ggctgttctg    1320
cgcaaaacac ggcatgtgaa cattctgctt ttcatggggt acatgacaaa ggacaacctg    1380
gcaattgtga cccagtggtg cgagggcagc agcctctaca aacacctgca tgtccaggag    1440
accaagtttc agatgttcca gctaattgac attgcccggc agacggctca gggaatggac    1500
tatttgcatg caaagaacat catccataga gacatgaaat ccaacaatat atttctccat    1560
gaaggcttaa cagtgaaaat tggagatttt ggtttggcaa cagtaaagtc acgctggagt    1620
ggttctcagc aggttgaaca acctactggc tctgtcctct ggatggcccc agaggtgatc    1680
cgaatgcagg ataacaaccc attcagtttc cagtcggatg tctactccta tggcatcgta    1740
ttgtatgaac tgatgacggg ggagcttcct tattctcaca tcaacaaccg agatcagatc    1800
atcttcatgg tgggccgagg atatgcctcc ccagatctta gtaagctata taagaactgc    1860
cccaaagcaa tgaagaggct ggtagctgac tgtgtgaaga aagtaaagga agaggaggct    1920
ctttttcccc agatcctgtc ttccattgag ctgctccaac actctctacc gaagatcaac    1980
cggagcgctt ccgagccatc cttgcatcgg gcagcccaca ctgaggatat caatgcttgc    2040
acgctgacca cgtccccgag gctgcctgtc ttctagttga ctttgcacct gtcttcaggc    2100
tgccagggga ggaggagaag ccagcaggca ccacttttct gctccctttc tccagaggca    2160
gaacacatgt tttcagagaa gctctgctaa ggaccttcta gactgctcac agggccttaa    2220
cttcatgttg ccttcttttc tatccctttg ggccctggga gaaggaagcc atttgcagtg    2280
ctggtgtgtc ctgctccctc cccacattcc ccatgctcaa ggcccagcct tctgtagatg    2340
cgcaagtgga tgttgatggt agtacaaaaa gcaggggccc agccccagct gttggctaca    2400
tgagtattta gaggaagtaa ggtagcaggc agtccagccc tgatgtggag acacatggga    2460
ttttggaaat cagcttctgg aggaatgcat gtcacaggcg ggactttctt cagagagtgg    2520
tgcagcgcca gacattttgc acataaggca ccaaacagcc caggactgcc gagactctgg    2580
ccgcccgaag gagcctgctt tggtactatg gaacttttct taggggacac gtcctccttt    2640
cacagcttct aaggtgtcca gtgcattggg atggttttcc aggcaaggca ctcggccaat    2700
ccgcatctca gccctctcag gagcagtctt ccatcatgct gaattttgtc ttccaggagc    2760
tgcccctatg gggcgggccg cagggccagc ctgtttctct aacaaacaaa caaacaaaca    2820
gccttgtttc tctagtcaca tcatgtgtat acaaggaagc caggaataca ggttttcttg    2880
atgatttggg ttttaatttt gtttttattg cacctgacaa aatacagtta tctgatggtc    2940
cctcaattat gttattttaa taaaataaat taaattt                            2977
```

<210> 16
<211> 813
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 16

```
Met Ser Arg Ile Asn Phe Lys Lys Ser Ser Ala Ser Thr Thr Pro Thr
 1               5                  10                  15
Ser Pro His Cys Pro Ser Pro Arg Leu Ile Ser Leu Pro Arg Cys Ala
            20                  25                  30
Ser Ser Ser Ile Asp Arg Lys Asp Gln Ala Ser Pro Met Ala Ser Pro
        35                  40                  45
Ser Thr Pro Leu Tyr Pro Lys His Ser Asp Ser Leu His Ser Leu Ser
    50                  55                  60
Gly His His Ser Ala Gly Gly Ala Gly Thr Ser Asp Lys Glu Pro Pro
65                  70                  75                  80
Lys Phe Lys Tyr Lys Met Ile Met Val His Leu Pro Phe Asp Gln His
                85                  90                  95
Ser Arg Val Glu Val Arg Pro Gly Glu Thr Ala Arg Asp Ala Ile Ser
            100                 105                 110
```

```
Lys Leu Leu Lys Lys Arg Asn Ile Thr Pro Gln Leu Cys His Val Asn
        115                 120                 125
Ala Ser Ser Asp Pro Lys Gln Glu Ser Ile Glu Leu Ser Leu Thr Met
    130                 135                 140
Glu Glu Ile Ala Ser Arg Leu Pro Gly Asn Glu Leu Trp Val His Ser
145                 150                 155                 160
Glu Tyr Leu Asn Thr Val Ser Ser Ile Lys His Ala Ile Val Arg Arg
                165                 170                 175
Thr Phe Ile Pro Pro Lys Ser Cys Asp Val Cys Asn Asn Pro Ile Trp
            180                 185                 190
Met Met Gly Phe Arg Cys Glu Phe Cys Gln Phe Lys Phe His Gln Arg
        195                 200                 205
Cys Ser Ser Phe Ala Pro Leu Tyr Cys Asp Leu Leu Gln Ser Val Pro
    210                 215                 220
Lys Asn Glu Asp Leu Val Lys Glu Leu Phe Gly Ile Ala Ser Gln Val
225                 230                 235                 240
Glu Gly Pro Asp Arg Ser Val Ala Glu Ile Val Leu Ala Asn Leu Ala
                245                 250                 255
Pro Thr Ser Gly Gln Ser Pro Ala Ala Thr Pro Asp Ser Ser His Pro
            260                 265                 270
Asp Leu Thr Ser Ile Lys Arg Thr Gly Gly Val Lys Arg His Pro Met
        275                 280                 285
Ala Val Ser Pro Gln Asn Glu Thr Ser Gln Leu Ser Pro Ser Gly Pro
    290                 295                 300
Tyr Pro Arg Asp Arg Ser Ser Ser Ala Pro Asn Ile Asn Ala Ile Asn
305                 310                 315                 320
Asp Glu Ala Thr Val Gln His Asn Gln Arg Ile Leu Asp Ala Leu Glu
                325                 330                 335
Ala Gln Arg Leu Glu Glu Glu Ser Arg Asp Lys Thr Gly Ser Leu Leu
            340                 345                 350
Ser Thr Gln Ala Arg His Arg Pro His Phe Gln Ser Gly His Ile Leu
        355                 360                 365
Ser Gly Ala Arg Met Asn Arg Leu His Pro Leu Val Asp Cys Thr Pro
    370                 375                 380
Leu Gly Ser Asn Ser Pro Ser Ser Thr Cys Ser Ser Pro Pro Gly Gly
385                 390                 395                 400
Leu Ile Gly Gln Pro Thr Leu Gly Gln Ser Pro Asn Val Ser Gly Ser
                405                 410                 415
Thr Thr Ser Ser Leu Val Ala Ala His Leu His Thr Leu Pro Leu Thr
            420                 425                 430
Pro Pro Gln Ser Ala Pro Pro Gln Lys Ile Ser Pro Gly Phe Phe Arg
        435                 440                 445
Asn Arg Ser Arg Ser Pro Gly Glu Arg Leu Asp Ala Gln Arg Pro Arg
    450                 455                 460
Pro Pro Gln Lys Pro His His Glu Asp Trp Glu Ile Leu Pro Asn Glu
465                 470                 475                 480
Phe Ile Ile Gln Tyr Lys Val Gly Ser Gly Ser Phe Gly Thr Val Tyr
                485                 490                 495
Arg Gly Glu Phe Phe Gly Thr Val Ala Ile Lys Lys Leu Asn Val Val
            500                 505                 510
Asp Pro Thr Pro Ser Gln Met Ala Ala Phe Lys Asn Glu Val Ala Val
        515                 520                 525
Leu Lys Lys Thr Arg His Leu Asn Val Leu Leu Phe Met Gly Trp Val
    530                 535                 540
Arg Glu Pro Glu Ile Ala Ile Ile Thr Gln Trp Cys Glu Gly Ser Ser
545                 550                 555                 560
Leu Tyr Arg His Ile His Val Gln Glu Pro Arg Val Glu Phe Glu Met
                565                 570                 575
```

```
Gly Ala Ile Ile Asp Ile Leu Lys Gln Val Ser Leu Gly Met Asn Tyr
            580                 585                 590
Leu His Ser Lys Asn Ile Ile His Arg Asp Leu Lys Thr Asn Asn Ile
        595                 600                 605
Phe Leu Met Asp Asp Met Ser Thr Val Lys Ile Gly Asp Phe Gly Leu
    610                 615                 620
Ala Thr Val Lys Thr Lys Trp Thr Val Asn Gly Gly Gln Gln Gln Gln
625                 630                 635                 640
Gln Pro Thr Gly Ser Ile Leu Trp Met Ala Pro Glu Val Ile Arg Met
                645                 650                 655
Gln Asp Asp Asn Pro Tyr Thr Pro Gln Ser Asp Val Tyr Ser Phe Gly
            660                 665                 670
Ile Cys Met Tyr Glu Ile Leu Ser Ser His Leu Pro Tyr Ser Asn Ile
        675                 680                 685
Asn Asn Arg Asp Gln Ile Leu Phe Met Val Gly Arg Gly Tyr Leu Arg
    690                 695                 700
Pro Asp Arg Ser Lys Ile Arg His Asp Thr Pro Lys Ser Met Leu Lys
705                 710                 715                 720
Leu Tyr Asp Asn Cys Ile Met Phe Asp Arg Asn Glu Arg Pro Val Phe
                725                 730                 735
Gly Glu Val Leu Glu Arg Leu Arg Asp Ile Ile Leu Pro Lys Leu Thr
            740                 745                 750
Arg Ser Gln Ser Ala Pro Asn Val Leu His Leu Asp Ser Gln Tyr Ser
        755                 760                 765
Val Met Asp Ala Val Met Arg Ser Gln Met Leu Ser Trp Ser Tyr Ile
    770                 775                 780
Pro Pro Ala Thr Ala Lys Thr Pro Gln Ser Ala Ala Ala Ala Ala Ala
785                 790                 795                 800
Arg Asn Lys Lys Ala Tyr Tyr Asn Val Tyr Gly Leu Ile
                805                 810
```

<210> 17
<211> 1044
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 17

```
atggagagag acttcgacct tggcatgggc agacctggcg ggctcggagg acttggtggt      60
gaaccgatca tgcaacaaat gccacagcca gcgcctcatc atccatcccg tagtagtaac     120
gaccacaatg tgaagaacct catgaagcag gccgaggaga actccggata tctcacattg     180
caaggtaacc gtcgtaaagc tgacttgaag gagcttcagt tcgtggaaga tattggtcat     240
ggaagctgcg gtacggtcac aaagtgcaga tacaagagtg tgatcatggc tgtgaagacg     300
atgcctcgga cgtcaaacag ttatgaaatg tcccgcattt tgatggatct tgacgtcatc     360
tgtctctctt tcgactgtcc gtacattgta cgttgcttcg gatacttcat caccaacttc     420
gacgtccgtg tctgcatgga gtgcatggct acttgccttg accgtctgct tatccgcatc     480
aagcagccaa ttccagagag aattattgga aagttgagtg tgagcatcat taaagctctg     540
cactacttga aaaccaagca ccaaatcatg caccgtgatg tgaagccatc aaacattctc     600
ctcgactgga gtggcgtcat caagctttgc gatttcggta ttgctggcag actgatcgag     660
tctcgtgctc attcgaagca agccggatgc cctctgtaca tgggtcctga gcgcctcgac     720
cccaacaact ttgactcgta tgacattcgc agtgacgtgt ggtcttttgg tgttactttg     780
gtcgagctgg caaccggaca gtacccatac gccggaaccg aattcgacat gatgtccaag     840
attctcaatg acgagccacc gcgcctggat ccggccaaat tctctccgga cttctgtcaa     900
ctcgtcgaga gctgcctgca gcgtgatcca acgatgcgtc ccaattacga tatgctcctc     960
cagcatccgt ttgtcgtgca tcacgagaaa attgaaaccg acgtcgagga gtggtttgcc    1020
gatgtgatgg gcgagtgcgg ataa                                           1044
```

<210> 18
<211> 1493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 18
Met Ala Ala Ala Ala Gly Asp Arg Ala Ser Ser Ser Gly Phe Pro Gly
1 5 10 15
Ala Ala Ala Ala Ser Pro Glu Ala Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30
Ala Leu Gln Gly Ser Gly Ala Pro Ala Ala Gly Ala Ala Gly Leu Leu
35 40 45
Arg Glu Pro Gly Ser Ala Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg
50 55 60
Gln Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln
65 70 75 80
Pro Leu Phe Leu Ala Ala Ala Ser Pro Pro Cys Pro Ser Thr Ser Pro
85 90 95
Ser Pro Glu Pro Ala Asp Ala Ala Ala Gly Ala Ser Arg Phe Gln Pro
100 105 110
Ala Ala Gly Pro Pro Pro Pro Gly Ala Ala Ser Arg Cys Gly Ser His
115 120 125
Ser Ala Glu Leu Ala Ala Ala Arg Asp Ser Gly Ala Arg Ser Pro Ala
130 135 140
Gly Ala Glu Pro Pro Ser Ala Ala Ala Pro Ser Gly Arg Glu Met Glu
145 150 155 160
Asn Lys Glu Thr Leu Lys Gly Leu His Lys Met Glu Asp Arg Pro Glu
165 170 175
Glu Arg Met Ile Arg Glu Lys Leu Lys Ala Thr Cys Met Pro Ala Trp
180 185 190
Lys His Glu Trp Leu Glu Arg Arg Asn Arg Arg Gly Pro Val Val Val
195 200 205
Lys Pro Ile Pro Ile Lys Gly Asp Gly Ser Glu Val Asn Asn Leu Ala
210 215 220
Ala Glu Pro Gln Gly Glu Gly Gln Ala Gly Ser Ala Ala Pro Ala Pro
225 230 235 240
Lys Gly Arg Arg Ser Pro Ser Pro Gly Ser Ser Pro Ser Gly Arg Ser
245 250 255
Val Lys Pro Glu Ser Pro Gly Val Arg Arg Lys Arg Val Ser Pro Val
260 265 270
Pro Phe Gln Ser Gly Arg Ile Thr Pro Pro Arg Arg Ala Pro Ser Pro
275 280 285
Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Ser Arg Arg Val Asn
290 295 300
Lys Val Met Arg Ala Arg Leu Tyr Leu Leu Gln Gln Ile Gly Pro Asn
305 310 315 320
Ser Phe Leu Ile Gly Gly Asp Ser Pro Asp Asn Lys Tyr Arg Val Phe
325 330 335
Ile Gly Pro Gln Asn Cys Ser Cys Gly Arg Gly Ala Phe Cys Ile His
340 345 350
Leu Leu Phe Val Met Leu Arg Val Phe Gln Leu Glu Pro Ser Asp Pro
355 360 365
Met Leu Trp Arg Lys Thr Leu Lys Asn Phe Glu Val Glu Ser Leu Phe
370 375 380

```
Gln Lys Tyr His Ser Arg Arg Ser Ser Arg Ile Lys Ala Pro Ser Arg
385                 390                 395                 400
Asn Thr Ile Gln Lys Phe Val Ser Arg Met Ser Asn Ser His Thr Leu
                405                 410                 415
Ser Ser Ser Ser Thr Ser Thr Ser Ser Ser Glu Asn Ser Ile Lys Asp
            420                 425                 430
Glu Glu Glu Gln Met Cys Pro Ile Cys Leu Leu Gly Met Leu Asp Glu
        435                 440                 445
Glu Ser Leu Thr Val Cys Glu Asp Gly Cys Arg Asn Lys Leu His His
    450                 455                 460
His Cys Met Ser Ile Trp Ala Glu Glu Cys Arg Arg Asn Arg Glu Pro
465                 470                 475                 480
Leu Ile Cys Pro Leu Cys Arg Ser Lys Trp Arg Ser His Asp Phe Tyr
                485                 490                 495
Ser His Glu Leu Ser Ser Pro Val Glu Ser Pro Ala Ser Leu Arg Ala
            500                 505                 510
Val Gln Gln Pro Ser Ser Pro Gln Gln Pro Val Ala Gly Ser Gln Arg
        515                 520                 525
Arg Asn Gln Glu Ser Ser Phe Asn Leu Thr His Phe Gly Thr Gln Gln
    530                 535                 540
Ile Pro Ser Ala Tyr Lys Asp Leu Ala Glu Pro Trp Ile Gln Val Phe
545                 550                 555                 560
Gly Met Glu Leu Val Gly Cys Leu Phe Ser Arg Asn Trp Asn Val Arg
                565                 570                 575
Glu Met Ala Leu Arg Arg Leu Ser His Asp Val Ser Gly Ala Leu Leu
            580                 585                 590
Leu Ala Asn Gly Glu Ser Thr Gly Asn Ser Gly Gly Gly Ser Gly Gly
        595                 600                 605
Ser Leu Ser Ala Gly Ala Ala Ser Gly Ser Ser Gln Pro Ser Ile Ser
    610                 615                 620
Gly Asp Val Val Glu Ala Cys Cys Ser Val Leu Ser Ile Val Cys Ala
625                 630                 635                 640
Asp Pro Val Tyr Lys Val Tyr Val Ala Ala Leu Lys Thr Leu Arg Ala
                645                 650                 655
Met Leu Val Tyr Thr Pro Cys His Ser Leu Ala Glu Arg Ile Lys Leu
            660                 665                 670
Gln Arg Leu Leu Arg Pro Val Val Asp Thr Ile Leu Val Lys Cys Ala
        675                 680                 685
Asp Ala Asn Ser Arg Thr Ser Gln Leu Ser Ile Ser Thr Val Leu Glu
    690                 695                 700
Leu Cys Lys Gly Gln Ala Gly Glu Leu Ala Val Gly Arg Glu Ile Leu
705                 710                 715                 720
Lys Ala Gly Ser Ile Gly Val Gly Gly Val Asp Tyr Val Leu Ser Cys
                725                 730                 735
Ile Leu Gly Asn Gln Ala Glu Ser Asn Asn Trp Gln Glu Leu Leu Gly
            740                 745                 750
Arg Leu Cys Leu Ile Asp Arg Leu Leu Leu Glu Phe Pro Ala Glu Phe
        755                 760                 765
Tyr Pro His Ile Val Ser Thr Asp Val Ser Gln Ala Glu Pro Val Glu
    770                 775                 780
Ile Arg Tyr Lys Lys Leu Leu Ser Leu Leu Thr Phe Ala Leu Gln Ser
785                 790                 795                 800
Ile Asp Asn Ser His Ser Met Val Gly Lys Leu Ser Arg Arg Ile Tyr
                805                 810                 815
Leu Ser Ser Ala Arg Met Val Thr Ala Val Pro Ala Val Phe Ser Lys
            820                 825                 830
Leu Val Thr Met Leu Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met
        835                 840                 845
```

```
Arg Arg Arg Leu Met Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val
    850                 855                 860
Ile Gln Leu Gly Val Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu
865                 870                 875                 880
Gln Ala Val Ala Pro Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His
                885                 890                 895
Thr Val His Arg Glu Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu
            900                 905                 910
Ser Ala Ser Ser Glu Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val
        915                 920                 925
Gly Leu Pro Ser Ser Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln
    930                 935                 940
Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser
945                 950                 955                 960
His Ala Gln Leu Met Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala
                965                 970                 975
Pro Ser Val Pro Asp Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro
            980                 985                 990
Cys Lys Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu
        995                 1000                1005
Gln Phe Gln Arg Asn Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser
    1010                1015                1020
Pro Val Phe Thr Gln Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg
1025                1030                1035                1040
Pro Lys Pro Ser Arg Pro Val Pro Gly Ser Thr Ser Lys Leu Gly Asp
                1045                1050                1055
Ala Thr Lys Ser Ser Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys
            1060                1065                1070
Asp Asp Ser Phe Gly Gly Gly Gly Asn Ser Gly Asn Ala Val Ile Pro
        1075                1080                1085
Ser Asp Glu Thr Val Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp
    1090                1095                1100
Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser
1105                1110                1115                1120
Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val Ala Val
                1125                1130                1135
Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val
            1140                1145                1150
Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu
        1155                1160                1165
Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro
    1170                1175                1180
Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile
1185                1190                1195                1200
Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln
                1205                1210                1215
Pro Tyr Arg Glu Asp Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu
            1220                1225                1230
Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr
        1235                1240                1245
Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu
    1250                1255                1260
Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly
1265                1270                1275                1280
His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu
                1285                1290                1295
Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val
            1300                1305                1310
```

Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile
1315 1320 1325
Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn
1330 1335 1340
Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser
1345 1350 1355 1360
Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu
1365 1370 1375
Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly
1380 1385 1390
Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly
1395 1400 1405
Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala
1410 1415 1420
Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His Leu Ala
1425 1430 1435 1440
Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser
1445 1450 1455
His Leu Ser Pro Gly Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu
1460 1465 1470
Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val
1475 1480 1485
Phe Arg Thr Thr Trp
1490

<210> 19
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 19
Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
1 5 10 15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
20 25 30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
35 40 45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
50 55 60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65 70 75 80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
85 90 95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
100 105 110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
115 120 125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
130 135 140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145 150 155 160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
165 170 175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
180 185 190

Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
195 200 205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
210 215 220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225 230 235 240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
245 250 255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
260 265 270
Leu Met Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
275 280 285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
290 295 300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305 310 315 320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
325 330 335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
340 345 350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
355 360 365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
370 375 380
Ser Thr Pro Thr His Ala Ala Gly Val
385 390

<210> 20
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 20
Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
1 5 10 15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
20 25 30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
35 40 45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
50 55 60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65 70 75 80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
85 90 95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
100 105 110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
115 120 125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
130 135 140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145 150 155 160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
165 170 175

```
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
            180                 185                 190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
        195                 200                 205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
    210                 215                 220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225                 230                 235                 240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
                245                 250                 255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
            260                 265                 270
Leu Leu Phe Gly Cys His Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
        275                 280                 285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
    290                 295                 300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305                 310                 315                 320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
                325                 330                 335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
            340                 345                 350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
        355                 360                 365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
    370                 375                 380
Ser Thr Pro Thr His Ala Ala Ser Ile
385                 390
```

<210> 21
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 21

```
Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1               5                  10                  15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
            20                  25                  30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
        35                  40                  45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
    50                  55                  60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65                  70                  75                  80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
                85                  90                  95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
            100                 105                 110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
        115                 120                 125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
    130                 135                 140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145                 150                 155                 160
```

```
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
                165                 170                 175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
            180                 185                 190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
        195                 200                 205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
    210                 215                 220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225                 230                 235                 240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
                245                 250                 255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
            260                 265                 270
Leu Met Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
        275                 280                 285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
    290                 295                 300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305                 310                 315                 320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
                325                 330                 335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
            340                 345                 350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
        355                 360                 365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
    370                 375                 380
Ser Thr Pro Thr His Ala Ala Gly Val
385                 390
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<210> 22
<211> 648
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 22

```
Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
 1                5                  10                  15
Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
            20                  25                  30
Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
        35                  40                  45
Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
    50                  55                  60
Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
65                  70                  75                  80
Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
                85                  90                  95
Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
            100                 105                 110
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
        115                 120                 125
Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
    130                 135                 140
```

```
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
145                 150                 155                 160
Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
                165                 170                 175
Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
            180                 185                 190
Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
        195                 200                 205
Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
    210                 215                 220
Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
225                 230                 235                 240
Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
                245                 250                 255
Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
            260                 265                 270
Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
        275                 280                 285
Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
    290                 295                 300
Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305                 310                 315                 320
Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
                325                 330                 335
Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
            340                 345                 350
Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
        355                 360                 365
His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
    370                 375                 380
Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385                 390                 395                 400
Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
                405                 410                 415
Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
            420                 425                 430
Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
        435                 440                 445
Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
    450                 455                 460
Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465                 470                 475                 480
Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
                485                 490                 495
Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
            500                 505                 510
Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
        515                 520                 525
Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
    530                 535                 540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545                 550                 555                 560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
                565                 570                 575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
            580                 585                 590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
        595                 600                 605
```

```
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
    610                 615                 620
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625                 630                 635                 640
Thr Ser Pro Arg Leu Pro Val Phe
                645
```